

SEQUENCE LISTINGS

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: COOPERATIVE RESEARCH CENTRE FOR TROPICAL PLANT
PATHOLOGY
10 (B) STREET: The University of Queensland
(C) CITY: St Lucia
(D) STATE: Queensland
(E) COUNTRY: Australia
15 (F) POSTAL CODE (ZIP): 4067

(ii) TITLE OF INVENTION: Antimicrobial Protein

(iii) NUMBER OF SEQUENCES: 28

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Macadamia integrifolia
40 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
1 5 10 15

Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
20 25 30

Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
35 40 45

Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
50 55 60

Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Glu Asp Pro Gln Thr

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Glu Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro
85 90 95

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Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
100 105 110

10

Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Tyr Glu Gln
115 120 125

Cys Gln Lys His Cys Gln Arg Arg Glu Thr Glu Pro Arg His Met Gln
130 135 140

15

Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
145 150 155 160

20

Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
165 170 175

25

Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
180 185 190

30

Glu Tyr Glu Asp Cys Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
195 200 205

35

Gln His Gln Cys Gln Leu Arg Cys Arg Glu Gln Gln Arg Gln His Gly
210 215 220

40

Arg Gly Gly Asp Met Met Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
225 230 235 240

45

Glu Glu Gly Glu Glu Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
245 250 255

50

Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
260 265 270

55

Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
275 280 285

Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
290 295 300

60

Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Ile Gly Gly Arg Gly
305 310 315 320

65

Ala Leu Lys Met Ile His His Asp Asn Arg Glu Ser Tyr Asn Leu Glu
325 330 335

70

Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
340 345 350

75

Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
355 360 365

Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
 370 375 380

Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
 5 385 390 395 400

Ala Leu Asn Thr Gln Thr Glu Lys Leu Arg Gly Val Phe Gly Gln Gln
 405 410 415

Arg Glu Gly Val Ile Ile Arg Ala Ser Gln Glu Gln Ile Arg Glu Leu
 10 420 425 430

Thr Arg Asp Asp Ser Glu Ser Arg His Trp His Ile Arg Arg Gly Gly
 15 435 440 445

Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
 450 455 460

Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
 20 465 470 475 480

Gln Leu Gln Asp Met Asp Leu Ser Val Phe Ile Ala Asn Val Thr Gln
 485 490 495

Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
 25 500 505 510

Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
 30 515 520 525

Ser Gly Arg His Gly Gly Arg Gly Gly Lys Arg His Glu Glu Glu
 530 535 540

Glu Asp Val His Tyr Glu Gln Val Arg Ala Arg Leu Ser Lys Arg Glu
 35 545 550 555 560

Ala Ile Val Val Leu Ala Gly His Pro Val Val Phe Val Ser Ser Gly
 565 570 575

Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
 40 580 585 590

His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
 45 595 600 605

Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
 610 615 620

Glu Glu Ser Phe Asn Ser Gln Asp Gln Ser Ile Phe Phe Pro Gly Pro
 50 625 630 635 640

Arg Gln His Gln Gln Gln Ser Pro Arg Ser Thr Lys Gln Gln Pro
 645 650 655

Leu Val Ser Ile Leu Asp Phe Val Gly Phe
 55 660 665

(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: cDNA
- 15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Macadamia integrifolia
 (F) TISSUE TYPE: Seeds
- 20 (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..85
- 25 (x) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 86..1999
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
- | | |
|---|-----|
| ATGGCGATCA ATACATCAAA TTTATGTTCT CTTCTCTTC TCCTTCACT CTTCCCTCTG | 60 |
| TCTACGACAG TGTCTCTTGC TGAAAGTGAA TTTGACAGGC AGGAATATGA GGAGTGCAAA | 120 |
| CGGCAATGCA TGCAGTTGGA GACATCAGGC CAGATGCGTC GGTGTGTGAG TCAGTGCGAT | 180 |
| AAGAGATTG AAGAGGATAT AGATTGGTCT AAGTATGATA ACCAAGAGGA TCCTCAGACG | 240 |
| GAATGCCAAC AATGCCAGAG GCGATGCAGG CAGCAGGAGA GTGGCCCACG TCAGCAACAA | 300 |
| TACTGCCAAC GACGCTGCAA GGAAATATGT GAAGAAGAAG AAGAATATAA CCGACAACGT | 360 |
| GATCCACAGC AGCAATACGA GCAATGTCAG AAGCACTGCC AACGGCGCGA GACAGAGCCA | 420 |
| CGTCACATGC AACATGTCA ACAACGCTGC GAGAGGAGAT ATGAAAAGGA GAAACGTAAG | 480 |
| CAACAAAAGA GATATGAAGA GCAACAACGT GAAGACGAAG AGAAATATGA AGAGCGAATG | 540 |
| AAGGAAGAAG ATAACAAACG CGATCCACAA CAAAGAGAGT ACGAAGACTG CCGGAGGCAGC | 600 |
| TGCGAACAAAC AGGAGCCACG TCAGCAGCAC CAGTGCCAGC TAAGATGCCG AGAGCAGCAG | 660 |
| AGGCAACACG GCCGAGGTGG CGATATGATG AACCCCTCAGA GGGGAGGCAG CGGCAGATAAC | 720 |
| GAGGAGGGAG AAGAGGAGCA AAGCGACAAC CCCTACTACT TCGACGAACG AAGCTTAAGT | 780 |
| ACAAGGTTCA GGACCGAGGA AGGCCACATC TCAGTTCTGG AGAACTTCTA TGGTAGATCC | 840 |
| AAGCTTCTAC GCGCACTAAA AAACTATCGC TTGGTGCTCC TCGAGGCTAA CCCCAACGCC | 900 |

| | | |
|----|---|------|
| | TTCGTGCTCC CTACCCACTT GGATGCAGAT GCCATTCTCT TGGTCATAGG AGGGAGAGGA | 960 |
| 5 | GCCCTCAAAA TGATCCACCA CGACAACAGA GAATCCTACA ACCTCGAGTG TGGAGACGTA | 1020 |
| | ATCAGAACATCC CAGCTGGAAC CACATTCTAC TTAATCAACC GAGACAACAA CGAGAGGCTC | 1080 |
| | CACATAGCCA AGTTCTTACA GACCATAATCC ACTCCTGGCC AATACAAGGA ATTCTTCCA | 1140 |
| 10 | GCTGGAGGCC AAAACCCAGA GCCGTACCTC AGTACCTTCA GCAAAGAGAT TCTCGAGGCT | 1200 |
| | GCGCTCAACA CACAAACAGA GAAGCTGCGT GGGGTGTTTG GACAGCAAAG GGAGGGAGTG | 1260 |
| 15 | ATAATTAGGG CGTCACAGGA GCAGATCAGG GAGTTGACTC GAGATGACTC AGAGTCACGA | 1320 |
| | CACTGGCATA TAAGGAGAGG TGGTGAATCA AGCAGGGGAC CTTACAATCT GTTCAACAAA | 1380 |
| | AGGCCACTGT ACTCCAACAA ATACGGTCAA GCCTACGAAG TCAAACCTGA GGACTACAGG | 1440 |
| 20 | CAACTCCAAG ACATGGACTT ATCGGTTTTC ATAGCCAACG TCACCCAGGG ATCCATGATG | 1500 |
| | GGTCCCCTCT TCAACACTAG GTCTACAAAG GTGGTAGTGG TGGCTAGTGG AGAGGCAGAT | 1560 |
| 25 | GTGGAAATGG CATGCCCTCA CTTGTCGGGA AGACACGGCG GCCGCGGTGG AGGAAAAGG | 1620 |
| | CATGAGGAGG AAGAGGATGT GCACTATGAG CAGGTTAGAG CACGTTGTC GAAGAGAGAG | 1680 |
| | GCCATTGTTG TTCTGGCAGG TCATCCCGTC GTCTCGTTT CATCCGGAAA CGAGAACCTG | 1740 |
| 30 | CTGCTTTTG CATTTGGAAT CAATGCCAA ACAACCACG AGAACTTCCT CGCGGGGAGA | 1800 |
| | GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA | 1860 |
| 35 | AGGAAAGAGG TAGAAGAGTC ATTTAACAGC CAGGACCAGT CTATCTTCTT TCCTGGGCC | 1920 |
| | AGGCAGCACCC AGAACAGTC GCCCCGCTCC ACCAAGCAAC AACAGCCTCT CGTCTCCATT | 1980 |
| | CTGGACTTCG TTGGCTTCTA AAGTTCCACA AAAAAGAGTG TGTTATGTAG TATAGGTTAG | 2040 |
| 40 | TAGCTCCTAG CTCGGTGTAT GAGAGTGGTA AGAGACTAAG ACGCTAAATC CCTAAGTAAC | 2100 |
| | TAACCTGGCG AGCTTGCCTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTTAAAAAAA | 2160 |
| 45 | AAAAAAAAAA A | 2171 |

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 666 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 55 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Macadamia integrifolia
(F) TISSUE TYPE: Seeds

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(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION:1..28

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(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:29..666

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
1 5 10 15

Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
20 25 30

Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
35 40 45

Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
50 55 60

Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Asp Asp Pro Gln Thr
65 70 75 80

Asp Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro
85 90 95

Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
100 105 110

Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Tyr Glu Gln
115 120 125

Cys Gln Glu Arg Cys Gln Arg His Glu Thr Glu Pro Arg His Met Gln
130 135 140

Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
145 150 155 160

Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
165 170 175

Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
180 185 190

Glu Tyr Glu Asp Cys Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
195 200 205

Gln Tyr Gln Cys Gln Arg Arg Cys Arg Glu Gln Gln Arg Gln His Gly
210 215 220

Arg Gly Gly Asp Leu Ile Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
 225 230 235 240

5 Glu Glu Gly Glu Lys Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
 245 250 255

Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
 10 260 265 270

Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
 15 275 280 285

Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
 290 295 300

Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Thr Gly Gly Arg Gly
 20 305 310 315 320

Ala Leu Lys Met Ile His Arg Asp Asn Arg Glu Ser Tyr Asn Leu Glu
 25 325 330 335

Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
 30 340 345 350

Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
 35 355 360 365

Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gln
 40 370 375 380

Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
 45 385 390 395 400

Ala Leu Asn Thr Gln Ala Glu Arg Leu Arg Gly Val Leu Gly Gln Gln
 50 405 410 415

Arg Glu Gly Val Ile Ile Ser Ala Ser Gln Glu Gln Ile Arg Glu Leu
 55 420 425 430

Thr Arg Asp Asp Ser Glu Ser Arg Arg Trp His Ile Arg Arg Gly Gly
 435 440 445

Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
 450 455 460

Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
 465 470 475 480

Gln Leu Gln Asp Met Asp Val Ser Val Phe Ile Ala Asn Ile Thr Gln
 500 505 510

Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
 55 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu

41

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Ser Gly Arg His Gly Gly Arg Arg Gly Gly Lys Arg His Glu Glu Glu
 530 535 540

5

Glu Asp Val His Tyr Glu Gln Val Lys Ala Arg Leu Ser Lys Arg Glu
 545 550 555 560

10

Ala Ile Val Val Pro Val Gly His Pro Val Val Phe Val Ser Ser Gly
 565 570 575

Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
 580 585 590

15

His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
 595 600 605

20

Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
 610 615 620

25

Glu Glu Leu Phe Asn Ser Gln Asp Glu Ser Ile Phe Phe Pro Gly Pro
 625 630 635 640

30

Arg Gln His Gln Gln Ser Ser Arg Ser Thr Lys Gln Gln Pro
 645 650 655

Leu Val Ser Ile Leu Asp Phe Val Gly Phe
 660 665

35

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Macadamia integrifolia
- (F) TISSUE TYPE: Seeds

45

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION:1..86

50

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:87..1999

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGGCGATCA ATACATCAAA TTTATGTTCT CTTCTCTTTC TCCTTCCCT CTTCCCTCTG

| | | |
|----|--|------|
| | TCAACGACAG TGTCTTTGC TGAAAGTGAA TTTGACAGGC AGGAATATGA GGAGTGCAA | 120 |
| 5 | CGGCAATGCA TGCAGTTGGA GACATCAGGC CAGATGCGTC GGTGTGTGAG TCAGTGCAT | 180 |
| | AAGAGATTTG AAGAGGATAT AGATTGGTCT AAGTATGATA ACCAAGACGA TCCTCAGACG | 240 |
| | GATTGCCAAC AATGCCAGAG GCGATGCAGG CAGCAGGAGA GTGGCCCACG TCAGCAACAA | 300 |
| 10 | TACTGCCAAC GACGCTGCAA GGAAATATGT GAAGAAGAAG AAGAATATAA CCGACAACGT | 360 |
| | GATCCACAGC AGCAATACGA GCAATGTCAG GAGCGCTGCC AACGGCACGA GACAGAGCCA | 420 |
| 15 | CGTCACATGC AAACATGTCA ACAACGCTGC GAGAGGAGAT ATGAAAAGGA GAAACGTAAG | 480 |
| | CAACAAAAGA GATATGAAGA GCAACAAACGT GAAGACGAAG AGAAATATGA AGAGCGAATG | 540 |
| | AAGGAAGAAG ATAACAAACG CGATCCACAA CAAAGAGAGT ACGAAGACTG CCGGAGGC | 600 |
| 20 | TGCGAACAAAC AGGAGCCACG TCAGCAGTAC CAGTGCCAGC GAAGATGCCG AGAGCAGCAG | 660 |
| | AGGCAACACG GCCGAGGTGG TGATTTGATT AACCTCTAGA GGGGAGGCAG CGGCAGATAC | 720 |
| 25 | GAGGAGGGAG AAGAGAAGCA AAGCGACAAC CCCTACTACT TCGACGAACG AAGCTTAAGT | 780 |
| | ACAAGGTTCA GGACCGAGGA AGGCCACATC TCAGTTCTGG AGAACTTCTA TGGTAGATCC | 840 |
| | AAGCTTCTAC GCGCACTAAA AACTATCGC TTGGTGCTCC TCGAGGCTAA CCCCAACGCC | 900 |
| 30 | TTCGTGCTCC CTACCCACTT GGACGCAGAT GCCATTCTCT TGGTCACCGG AGGGAGAGGA | 960 |
| | GCCCTCAAAA TGATCCACCG TGACAACAGA GAATCCTACA ACCTCGAGTG TGGAGACGTA | 1020 |
| 35 | ATCAGAATCC CAGCTGGAAC CACATTCTAC TTAATCAACC GAGACAACAA CGAGAGGCTC | 1080 |
| | CACATAGCCA AGTTCTTACA GACCATATCC ACTCCTGGCC AATACAAGGA ATTCTTCCCA | 1140 |
| | GCTGGAGGCC AAAACCCAGA GCCGTACCTC AGTACCTTCA GCAAAGAGAT TCTCGAGGCT | 1200 |
| 40 | GCGCTCAACA CACAAGCAGA GAGGCTGCGT GGGGTGCTTG GACAGCAAAG GGAGGGAGTG | 1260 |
| | ATAATTAGTG CGTCACAGGA GCAGATCAGG GAGTTGACTC GAGATGACTC AGAGTCACGA | 1320 |
| 45 | CGCTGGCATA TAAGGAGAGG TGGTGAATCA AGCAGGGGAC CTTACAATCT GTTCAACAAA | 1380 |
| | AGGCCACTGT ACTCCAACAA ATACGGTCAA GCCTACGAAG TCAAACCTGA GGACTACAGG | 1440 |
| | CAACTCCAAG ACATGGACGT ATCGGTTTTC ATAGCCAACA TCACCCAGGG ATCCATGATG | 1500 |
| 50 | GGTCCCTTCT TCAACACTAG GTCTACAAAG GTGGTAGTGG TGGCTAGTGG AGAGGCAGAT | 1560 |
| | GTGGAAATGG CATGCCCTCA CTTGTCGGGA AGACACGGCG GCCGCCGTGG AGGGAAAAGG | 1620 |
| 55 | CATGAGGAGG AAGAGGATGT GCACTATGAG CAGGTTAAAG CACGTTGTC GAAGAGAGAG | 1680 |
| | GCCATTGTTG TTCCGGTAGG TCATCCCGTC GTCTTCGTTT CATCCGGAAA CGAGAACCTG | 1740 |

| | | |
|----|--|------|
| | CTGCTTTTG CATTTGGAAT CAATGCCAA AACAAACCACG AGAACTTCCT CGCGGGGAGA | 1800 |
| 5 | GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA | 1860 |
| | AGGAAAGAGG TAGAACAGTT ATTTAACAGC CAGGACGAGT CTATCTTCTT TCCTGGGCC | 1920 |
| | AGGCAGCACC AGCAACAGTC TTCCCGCTCC ACCAACGAAAC AACAGCCTCT CGTCTCCATT | 1980 |
| 10 | CTGGACTTCG TTGGCTTCTA AAGTTCTACA AAAAAGAGTG TGTTATGTAG TATAGGTTAG | 2040 |
| | TAGCTCCTAG CTCGGTGTAT GCGAGTGGTA AGAGACCAAG ACGCTAAATC CCTAAGTAAC | 2100 |
| 15 | TAACCTGGCG AGCTTGCCTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTTAAAAAAA | 2160 |
| | AAAAAAAAAA A | 2171 |

(2) INFORMATION FOR SEQ ID NO: 5:

| | |
|----|--|
| 20 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 625 amino acids |
| | (B) TYPE: amino acid |
| 25 | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| | (ii) MOLECULE TYPE: protein |
| 30 | (vi) ORIGINAL SOURCE: |
| | (A) ORGANISM: Macadamia integrifolia |
| | (F) TISSUE TYPE: Seeds |
| 35 | (ix) FEATURE: |
| | (A) NAME/KEY: partial mat_peptide |
| | (B) LOCATION: 1..625 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: |
| 40 | Gln Cys Met Gln Leu Glu Thr Ser Gly Gln Met Arg Arg Cys Val Ser 1 5 10 15 |
| | Gln Cys Asp Lys Arg Phe Glu Glu Asp Ile Asp Trp Ser Lys Tyr Asp 20 25 30 |
| 45 | Asn Gln Glu Asp Pro Gln Thr Glu Cys Gln Gln Cys Gln Arg Arg Cys 35 40 45 |
| | Arg Gln Gln Glu Ser Asp Pro Arg Gln Gln Gln Tyr Cys Gln Arg Arg 50 55 60 |
| 50 | Cys Lys Glu Ile Cys Glu Glu Glu Glu Tyr Asn Arg Gln Arg Asp 65 70 75 80 |
| 55 | Pro Gln Gln Gln Tyr Glu Gln Cys Gln Lys Arg Cys Gln Arg Arg Glu 85 90 95 |

Thr Glu Pro Arg His Met Gln Ile Cys Gln Gln Arg Cys Glu Arg Arg
 100 105 110

5 Tyr Glu Lys Glu Lys Arg Lys Gln Gln Lys Arg Tyr Glu Glu Gln Gln
 115 120 125

Arg Glu Asp Glu Glu Lys Tyr Glu Glu Arg Met Lys Glu Gly Asp Asn
 130 135 140

10 Lys Arg Asp Pro Gln Gln Arg Glu Tyr Glu Asp Cys Arg Arg His Cys
 145 150 155 160

15 Glu Gln Gln Glu Pro Arg Leu Gln Tyr Gln Cys Gln Arg Arg Cys Gln
 165 170 175 180

Glu Gln Gln Arg Gln His Gly Arg Gly Gly Asp Leu Met Asn Pro Gln
 185 190 195

20 Arg Gly Gly Ser Gly Arg Tyr Glu Glu Gly Glu Glu Lys Gln Ser Asp
 200 205 210

Asn Pro Tyr Tyr Phe Asp Glu Arg Ser Leu Ser Thr Arg Phe Arg Thr
 215 220 225

25 Glu Glu Gly His Ile Ser Val Leu Glu Asn Phe Tyr Gly Arg Ser Lys
 230 235 240 245

Leu Leu Arg Ala Leu Lys Asn Tyr Arg Leu Val Leu Leu Glu Ala Asn
 250 255 260

30 Pro Asn Ala Phe Val Leu Pro Thr His Leu Asp Ala Asp Ala Ile Leu
 265 270 275

35 Leu Val Ile Gly Gly Arg Gly Ala Leu Lys Met Ile His Arg Asp Asn
 280 285 290

Arg Glu Ser Tyr Asn Leu Glu Cys Gly Asp Val Ile Arg Ile Pro Ala
 295 300 305

40 Gly Thr Thr Phe Tyr Leu Ile Asn Arg Asp Asn Asn Glu Arg Leu His
 310 315 320 325

Ile Ala Lys Phe Leu Gln Thr Ile Ser Thr Pro Gly Gln Tyr Lys Glu
 330 335 340

45 Phe Phe Pro Ala Gly Gly Gln Asn Pro Glu Pro Tyr Leu Ser Thr Phe
 345 350 355

Ser Lys Glu Ile Leu Glu Ala Ala Leu Asn Thr Gln Thr Glu Arg Leu
 360 365 370

Arg Gly Val Leu Gly Gln Gln Arg Glu Gly Val Ile Ile Arg Ala Ser
 375 380 385

55 Gln Glu Gln Ile Arg Glu Leu Thr Arg Asp Asp Ser Glu Ser Arg Arg
 390 395 400 405

Trp His Ile Arg Arg Gly Gly Glu Ser Ser Arg Gly Pro Tyr Asn Leu
410 415 420

5 Phe Asn Lys Arg Pro Leu Tyr Ser Asn Lys Tyr Gly Gln Ala Tyr Glu
425 430 435

Val Lys Pro Glu Asp Tyr Arg Gln Leu Gln Asp Met Asp Val Ser Val
10 440 445 450

Phe Ile Ala Asn Ile Thr Gln Gly Ser Met Met Gly Pro Phe Phe Asn
455 460 470

15 Thr Arg Ser Thr Lys Val Val Val Val Ala Ser Gly Glu Ala Asp Val
480 485 490 500

Glu Met Ala Cys Pro His Leu Ser Gly Arg His Gly Gly Arg Gly Gly
505 510 515

20 Gly Lys Arg His Glu Glu Glu Glu Val His Tyr Glu Gln Val Arg
520 525 530

Ala Arg Leu Ser Lys Arg Glu Ala Ile Val Val Leu Ala Gly His Pro
25 535 540 545

Val Val Phe Val Ser Ser Gly Asn Glu Asn Leu Leu Leu Phe Ala Phe
550 555 560

30 Gly Ile Asn Ala Gln Asn Asn His Glu Asn Phe Leu Ala Gly Arg Glu
565 570 575 580

Arg Asn Val Leu Gln Gln Ile Glu Pro Gln Ala Met Glu Leu Ala Phe
585 590 595

35 Ala Ala Ser Arg Lys Glu Val Glu Glu Leu Phe Asn Ser Gln Asp Glu
600 605 610

40 Ser Ile Phe Phe Pro Gly Pro Arg Gln His Gln Gln Ser Pro Arg
615 620 625

Ser Thr Lys Gln Gln Pro Leu Val Ser Ile Leu Asp Phe Val Gly
45 630 635 640
Phe

45 (2) INFORMATION FOR SEQ ID NO: 6:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Macadamia integrifolia

(F) TISSUE TYPE: Seeds

(x) FEATURE:

- 5 (A) NAME/KEY: partial mat_peptide
 (B) LOCATION:1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

| | | |
|----|---|------|
| | CAATGCATGC AGTTAGAGAC ATCAGGCCAG ATGCGTCGGT GTGTGAGTCA GTGCGATAAG | 60 |
| 10 | AGATTTGAAG AGGATATAGA TTGGTCTAAG TATGATAACC AAGAGGATCC TCAGACGGAA | 120 |
| | TGCCAACAAAT GCCAGAGGCG ATGCAGGCAG CAGGAGAGTG ACCCACGTCA GCAACAATAC | 180 |
| 15 | TGCCAACGAC GCTGCAAGGA AATATGTGAA GAAGAAGAAG AATATAACCG ACAACGTGAT | 240 |
| | CCACAGCAGC AATACGAGCA ATGTCAGAAG CGCTGCCAAC GGCGCGAGAC AGAGCCACGT | 300 |
| 20 | CACATGCAAA TATGTCAACA ACGCTGCGAG AGGAGATATG AAAAGGAGAA ACGTAAGCAA | 360 |
| | CAAAAGAGAT ATGAAGAGCA ACAACGTGAA GACGAAGAGA AATATGAAGA GCGAATGAAG | 420 |
| | GAAGGAGATA ACAAACGCGA TCCACAACAA AGAGAGTACG AAGACTGCCG GCGGCACTGC | 480 |
| 25 | GAACAAACAGG AGCCACGTCT GCAGTACCAAG TGCCAGCGAA GATGCCAAGA GCAGCAGAGG | 540 |
| | CAACACGGCC GAGGTGGCGA TTTGATGAAC CCTCAGAGGG GAGGCAGCGG CAGATACGAG | 600 |
| 30 | GAGGGAGAAG AGAACCAAAG CGACAACCCC TACTACTTCG ACGAACGAAG CTTAAGTACA | 660 |
| | AGGTTCAGGA CCGAGGAAGG CCACATCTCA GTTCTGGAGA ACTTCTATGG TAGATCCAAG | 720 |
| | CTTCTACGCG CACTAAAAAA CTATCGCTTG GTGCTCCTCG AGGCTAACCC CAACGCCTTC | 780 |
| 35 | GTGCTCCCTA CCCACTTGGG TGCAGATGCC ATTCTCTTGG TCATCGGAGG GAGAGGAGCC | 840 |
| | CTCAAAATGA TCCACCGTGA CAACAGAGAA TCCTACAACC TCGAGTGTGG AGACGTAATC | 900 |
| | AGAATCCCAG CTGGAACCAC ATTCTACTTA ATCAACCGAG ACAACAACGA GAGGCTCCAC | 960 |
| 40 | ATAGCCAAGT TCTTACAGAC CATATCCACT CCTGGCCAAT ACAAGGAATT CTTCCCAGCT | 1020 |
| | GGAGGCCAAA ACCCAGAGCC GTACCTCAGT ACCTTCAGCA AAGAGATTCT CGAGGCTGCG | 1080 |
| 45 | CTCAACACAC AAACAGAGAG GCTGCGTGGG GTGCTTGGAC AGCAAAGGGA GGGAGTGATA | 1140 |
| | ATTAGGGCGT CACAGGAGCA GATCAGGGAG TTGACTCGAG ATGACTCAGA GTCACGACGC | 1200 |
| | TGGCATATAA GGAGAGGTGG TGAATCAAGC AGGGGACCTT ACAATCTGTT CAACAAAAGG | 1260 |
| 50 | CCACTGTACT CCAACAAATA CGGTCAAGCC TACGAAGTCA AACCTGAGGA CTACAGGCAA | 1320 |
| | CTCCAAGACA TGGACGTATC AGTTTCATA GCCAACATCA CCCAGGGATC CATGATGGGT | 1380 |
| 55 | CCCTTCTTCA ACACTAGGTC TACAAAGGTG GTAGTGGTGG CTAGTGGAGA GGCAGATGTG | 1440 |

GAAATGGCAT GCCCTCACTT GTCGGGAAGA CACGGCGGCC GCGGTGGAGG GAAAAGGCAT 1500
 GAGGAGGAAG AGGAGGTGCA CTATGAGCAG GTTAGAGCAC GTTGTCGAA GAGAGAGGCC 1560
 5 ATTGTTGTTG TGGCAGGTCA TCCCCTCGTC TTCGTTTCAT CCGGAAACGA AAACCTGCTG 1620
 CTTTTGCAT TTGGAATCAA TGCCCAAAAC AACCACGAGA ACTTCCTCGC GGGGAGAGAG 1680
 10 AGGAACGTGC TGCAGCAGAT AGAGCCACAG GCAATGGAGC TAGCGTTGC CGCTTCAAGG 1740
 AAAGAGGTAG AAGAGTTATT TAACAGCCAG GACGAGTCTA TCTTCTTTCC TGGGCCAGG 1800
 CAGCACCAGC AACAGTCGCC CCGCTCCACC AAGCAACAAAC AGCCTCTCGT CTCCATTCTG 1860
 15 GACTTCGTTG GCTTCTAAAG TTCTACAAAAA AAGAGTGTGT TATGTAGTAT AGGTTAGTAG 1920
 CTCCTAGCTC GGTGTATGAG AGTGGTAAGA GACTAAGACG CTAAATCCCT AAGTAACTAA 1980
 20 CCTGGCGAGC TTGCGTGTAT GCAAATAAAG AGGAACAGCT TTCCAACCTT AGAAAGCTCT 2040
 TTTTTTTTTT TTTTTTCTTT CTTTTCTTA AGAAATAAAC GAACGTAGAT TGCGGCTCAA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2140

25 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Theobroma cacao
- (F) TISSUE TYPE: Seeds

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Val Ile Ser Lys Ser Pro Phe Ile Val Leu Ile Phe Ser Leu Leu
 1 5 10 15

45 Leu Ser Phe Ala Leu Leu Cys Ser Gly Val Ser Ala Tyr Gly Arg Lys
 20 25 30

Gln Tyr Glu Arg Asp Pro Arg Gln Gln Tyr Glu Gln Cys Gln Arg Arg
 35 40 45

50 Cys Glu Ser Glu Ala Thr Glu Glu Arg Glu Gln Glu Gln Cys Glu Gln
 55 60

55 Arg Cys Glu Arg Glu Tyr Lys Glu Gln Gln Arg Gln Gln Glu Glu Glu
 65 70 75 80

| | | | | |
|----|---|-----|-----|-----|
| | Leu Gln Arg Gln Tyr Gln Gln Cys Gln Gly Arg Cys Gln Glu Gln Gln | | | |
| | 85 | 90 | 95 | |
| 5 | Gln Gly Gln Arg Glu Gln Gln Cys Gln Arg Lys Cys Trp Glu Gln | | | |
| | 100 | 105 | 110 | |
| | Tyr Lys Glu Gln Glu Arg Gly Glu His Glu Asn Tyr His Asn His Lys | | | |
| | 115 | 120 | 125 | |
| 10 | Lys Asn Arg Ser Glu Glu Glu Gly Gln Gln Arg Asn Asn Pro Tyr | | | |
| | 130 | 135 | 140 | |
| 15 | Tyr Phe Pro Lys Arg Arg Ser Phe Gln Thr Arg Phe Arg Asp Glu Glu | | | |
| | 145 | 150 | 155 | 160 |
| | Gly Asn Phe Lys Ile Leu Gln Arg Phe Ala Glu Asn Ser Pro Pro Leu | | | |
| | 165 | 170 | 175 | |
| 20 | Lys Gly Ile Asn Asp Tyr Arg Leu Ala Met Phe Glu Ala Asn Pro Asn | | | |
| | 180 | 185 | 190 | |
| | Thr Phe Ile Leu Pro His His Cys Asp Ala Glu Ala Ile Tyr Phe Val | | | |
| | 195 | 200 | 205 | |
| 25 | Thr Asn Gly Lys Gly Thr Ile Thr Phe Val Thr His Glu Asn Lys Glu | | | |
| | 210 | 215 | 220 | |
| 30 | Ser Tyr Asn Val Gln Arg Gly Thr Val Val Ser Val Pro Ala Gly Ser | | | |
| | 225 | 230 | 235 | 240 |
| | Thr Val Tyr Val Val Ser Gln Asp Asn Gln Glu Lys Leu Thr Ile Ala | | | |
| | 245 | 250 | 255 | |
| 35 | Val Leu Ala Leu Pro Val Asn Ser Pro Gly Lys Tyr Glu Leu Phe Phe | | | |
| | 260 | 265 | 270 | |
| | Pro Ala Gly Asn Asn Lys Pro Glu Ser Tyr Tyr Gly Ala Phe Ser Tyr | | | |
| | 275 | 280 | 285 | |
| 40 | Glu Val Leu Glu Thr Val Phe Asn Thr Gln Arg Glu Lys Leu Glu Glu | | | |
| | 290 | 295 | 300 | |
| | Ile Leu Glu Glu Gln Arg Gly Gln Lys Arg Gln Gln Gly Gln Gln Gly | | | |
| 45 | 305 | 310 | 315 | 320 |
| | Met Phe Arg Lys Ala Lys Pro Glu Gln Ile Arg Ala Ile Ser Gln Gln | | | |
| | 325 | 330 | 335 | |
| 50 | Ala Thr Ser Pro Arg His Arg Gly Glu Arg Leu Ala Ile Asn Leu | | | |
| | 340 | 345 | 350 | |
| | Leu Ser Gln Ser Pro Val Tyr Ser Asn Gln Asn Gly Arg Phe Phe Glu | | | |
| | 355 | 360 | 365 | |
| 55 | Ala Cys Pro Glu Asp Phe Ser Gln Phe Gln Asn Met Asp Val Ala Val | | | |
| | 370 | 375 | 380 | |

Ser Ala Phe Lys Leu Asn Gln Gly Ala Ile Phe Val Pro His Tyr Asn
385 390 395 400

5 Ser Lys Ala Thr Phe Val Val Phe Val Thr Asp Gly Tyr Gly Tyr Ala
405 410 415

Gln Met Ala Cys Pro His Leu Ser Arg Gln Ser Gln Gly Ser Gln Ser
10 420 425 430

Gly Arg Gln Asp Arg Arg Glu Gln Glu Glu Glu Ser Glu Glu Glu Thr
15 435 440 445

Phe Gly Glu Phe Gln Gln Val Lys Ala Pro Leu Ser Pro Gly Asp Val
15 450 455 460

Phe Val Ala Pro Ala Gly His Ala Val Thr Phe Phe Ala Ser Lys Asp
20 465 470 475 480

Gln Pro Leu Asn Ala Val Ala Phe Gly Leu Asn Ala Gln Asn Asn Gln
25 485 490 495

Arg Ile Phe Leu Ala Gly Arg Pro Phe Phe Leu Asn His Lys Gln Asn
25 500 505 510

Thr Asn Val Ile Lys Phe Thr Val Lys Ala Ser Ala Tyr
30 515 520 525

30 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gossypium hirsutum*
- (F) TISSUE TYPE: Seeds

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Val Arg Asn Lys Ser Ala Cys Val Val Leu Leu Phe Ser Leu Phe
1 5 10 15

Leu Ser Phe Gly Leu Leu Cys Ser Ala Lys Asp Phe Pro Gly Arg Arg
50 20 25 30

Gly Asp Asp Asp Pro Pro Lys Arg Tyr Glu Asp Cys Arg Arg Arg Cys
35 40 45

55 Glu Trp Asp Thr Arg Gly Gln Lys Glu Gln Gln Cys Glu Glu Ser
50 55 60

| | | | | |
|----|---|-----|-----|-----|
| | Cys Lys Ser Gln Tyr Gly Glu Lys Asp Gln Gln Gln Arg His Arg Pro | | | |
| 65 | 70 | 75 | 80 | |
| 5 | Glu Asp Pro Gln Arg Arg Tyr Glu Glu Cys Gln Gln Glu Cys Arg Gln | | | |
| | 85 | 90 | 95 | |
| 10 | Gln Glu Glu Arg Gln Gln Pro Gln Cys Gln Gln Arg Cys Leu Lys Arg | | | |
| | 100 | 105 | 110 | |
| 15 | Phe Glu Gln Glu Gln Gln Ser Gln Arg Gln Phe Gln Glu Cys Gln | | | |
| | 115 | 120 | 125 | |
| 20 | Gln His Cys His Gln Gln Glu Gln Arg Pro Glu Lys Lys Gln Gln Cys | | | |
| | 130 | 135 | 140 | |
| 25 | Val Arg Glu Cys Arg Glu Lys Tyr Gln Glu Asn Pro Trp Arg Gly Glu | | | |
| | 145 | 150 | 155 | 160 |
| 30 | Arg Glu Glu Glu Ala Glu Glu Glu Thr Glu Glu Gly Glu Gln Glu | | | |
| | 165 | 170 | 175 | |
| 35 | Gln Ser His Asn Pro Phe His Phe His Arg Arg Ser Phe Gln Ser Arg | | | |
| | 180 | 185 | 190 | |
| 40 | Phe Arg Glu Glu His Gly Asn Phe Arg Val Leu Gln Arg Phe Ala Ser | | | |
| | 195 | 200 | 205 | |
| 45 | Arg His Pro Ile Leu Arg Gly Ile Asn Glu Phe Arg Leu Ser Ile Leu | | | |
| | 210 | 215 | 220 | |
| 50 | Glu Ala Asn Pro Asn Thr Phe Val Leu Pro His His Cys Asp Ala Glu | | | |
| | 225 | 230 | 235 | 240 |
| 55 | Lys Ile Tyr Leu Val Thr Asn Gly Arg Gly Thr Leu Thr Phe Leu Thr | | | |
| | 245 | 250 | 255 | |
| 60 | His Glu Asn Lys Glu Ser Tyr Asn Ile Val Pro Gly Val Val Val Lys | | | |
| | 260 | 265 | 270 | |
| 65 | Val Pro Ala Gly Ser Thr Val Tyr Leu Ala Asn Gln Asp Asn Lys Glu | | | |
| | 275 | 280 | 285 | |
| 70 | Lys Leu Ile Ile Ala Val Leu His Arg Pro Val Asn Asn Pro Gly Gln | | | |
| | 290 | 295 | 300 | |
| 75 | Phe Glu Glu Phe Phe Pro Ala Gly Ser Gln Arg Pro Gln Ser Tyr Leu | | | |
| | 305 | 310 | 315 | 320 |
| 80 | Arg Ala Phe Ser Arg Glu Ile Leu Glu Pro Ala Phe Asn Thr Arg Ser | | | |
| | 325 | 330 | 335 | |
| 85 | Glu Gln Leu Asp Glu Leu Phe Gly Gly Arg Gln Ser Arg Arg Gln | | | |
| | 340 | 345 | 350 | |
| 90 | Gln Gly Gln Gly Met Phe Arg Lys Ala Ser Gln Glu Gln Ile Arg Ala | | | |

51

355

360

365

Leu Ser Gln Glu Ala Thr Ser Pro Arg Glu Lys Ser Gly Glu Arg Phe
370 375 380

5

Ala Phe Asn Leu Leu Ser Gln Thr Pro Arg Tyr Ser Asn Gln Asn Gly
385 390 395 400

10

Arg Phe Phe Glu Ala Cys Pro Pro Glu Phe Arg Gln Leu Arg Asp Ile
405 410 415

Asn Val Thr Val Ser Ala Leu Gln Leu Asn Gln Gly Ser Ile Phe Val
420 425 430

15

Pro His Tyr Asn Ser Lys Ala Thr Phe Val Ile Leu Val Thr Glu Gly
435 440 445

20

Asn Gly Tyr Ala Glu Met Val Ser Pro His Leu Pro Arg Gln Ser Ser
450 455 460

Tyr Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Gln Glu Gln Glu
465 470 475 480

25

Glu Glu Arg Arg Ser Gly Gln Tyr Arg Lys Ile Arg Ser Arg Leu Ser
485 490 495

30

Arg Gly Asp Ile Phe Val Val Pro Ala Asn Phe Pro Val Thr Phe Val
500 505 510

Ala Ser Gln Asn Gln Asn Leu Arg Met Thr Gly Phe Gly Leu Tyr Asn
515 520 525

35

Gln Asn Ile Asn Pro Asp His Asn Gln Arg Ile Phe Val Ala Gly Lys
530 535 540

Ile Asn His Val Arg Gln Trp Asp Ser Gln Ala Lys Glu Leu Ala Phe
545 550 555 560

40

Gly Val Ser Ser Arg Leu Val Asp Glu Ile Phe Asn Ser Asn Pro Gln
565 570 575

Glu Ser Tyr Phe Val Ser Arg Gln Arg Gln Arg Ala Ser Glu
580 585 590

45 (2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

52

Arg Gln Arg Asp Pro Gln Gln Ala Glu Gln Ala Gln Lys Arg Ala
1 5 10 15

Gln Arg Arg Glu Thr Glu
5 20

(2) INFORMATION FOR SEQ ID NO: 10:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

20 Pro Arg His Met Gln Ile Ala Gln Gln Arg Ala Glu Arg Arg Ala Glu
1 5 10 15

Lys Glu Lys Arg Lys Gln Gln Lys Arg
20 25

(2) INFORMATION FOR SEQ ID NO: 11:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

35 Met Ala Trp Phe His Val Ser Val Cys Asn Ala Val Phe Val Val Ile
1 5 10 15

40 Ile Ile Ile Met Leu Leu Met Phe Val Pro Val Val Arg Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO: 12:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: nucleotide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CAGCAGCAGT ATGAGCAGTG

20

5 (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TTTTTCGTAK CKKCKTTCGC A

21

20 (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ACACCATATG CGACAACGTG ATCC

24

35 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGTTGTTTTC TCTATTCCCTA GGGTTG

26

50 (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

5 Met Gly His His His His His His His His His Ser Ser Gly His
1 5 10 15

10 Ile Glu Gly Arg His Met
20

(2) INFORMATION FOR SEQ ID NO: 17:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

25 GGGATTCCA TATGTATGAG CGTGATCCTC GACAGCAATA CGAGCAATGC CAGAGGCGAT 60
GCGAGTCGGA AGCGACTGAA GAAAGGGAGC 90

30 (2) INFORMATION FOR SEQ ID NO: 18

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GAAGCGACTG AAGAAAAGGGA GCAAGAGCAG TGTGAACAAC GCTGTGAAAG GGAGTACAAG 60
GAGCAGCAGA GACAGCAATA GGGATCCACA C 91

45 (2) INFORMATION FOR SEQ ID NO: 19

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGAATTCCA TATGCTTCAA AGGCAATACC AGCAATGTCA AGGGCGTTGT CAAGAGCAAC 60
5 AACAGGGGCA GAGAGAGCAG CAGCAGTGCC AGAGAAAATG C 101

(2) INFORMATION FOR SEQ ID NO: 20

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

20 GTGTGGATCC CTAGCTCCTA TTTTTTTTGT GATTATGGTA ATTCTCGTGC TCGCCTCTCT 60
CTTGTTCCTT ATATTGCTCC CAGCATTTC TCTGGCACTG CT 102

25 (2) INFORMATION FOR SEQ ID NO: 21:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Peanut
(F) TISSUE TYPE: Seeds

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Arg Gly Arg Val Ser Pro Leu Met Leu Leu Leu Gly Ile Leu Val
1 5 10 15

45 Leu Ala Ser Val Ser Ala Thr Gln Ala Lys Ser Pro Tyr Arg Lys Thr
20 25 30

Glu Asn Pro Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln Glu Pro
35 40 45

50 Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys Leu Glu
50 55 60

55 Tyr Asp Pro Arg Cys Val Tyr Asp Thr Gly Ala Thr Asn Gln Arg His
65 70 75 80

Pro Pro Gly Glu Arg Thr Arg Gly Arg Gln Pro Gly Asp Tyr Asp Asp
 85 90 95

5 Asp Arg Arg Gln Pro Arg Arg Glu Glu Gly Gly Arg Trp Gly Pro Ala
 100 105 110

Glu Pro Arg Glu Arg Glu Glu Asp Trp Arg Gln Pro Arg Glu
 115 120 125

10 Asp Trp Arg Arg Pro Ser His Gln Gln Pro Arg Lys Ile Arg Pro Glu
 130 135 140

Gly Arg Glu Gly Glu Gln Glu Trp Gly Thr Pro Gly Ser Glu Val Arg
 145 150 155 160

15 Glu Glu Thr Ser Arg Asn Asn Pro Phe Tyr Phe Pro Ser Arg Arg Phe
 165 170 175 180

20 Ser Thr Arg Tyr Gly Asn Gln Asn Gly Arg Ile Arg Val Leu Gln Arg
 185 190 195

Phe Asp Gln Arg Ser Lys Gln Phe Gln Asn Leu Gln Asn His Arg Ile
 200 205 210

25 Val Gln Ile Glu Ala Arg Pro Asn Thr Leu Val Leu Pro Lys His Ala
 215 220 225

Asp Ala Asp Asn Ile Leu Val Ile Gln Gln Gly Gln Ala Thr Val Thr
 230 235 240 245

30 Val Ala Asn Gly Asn Asn Arg Lys Ser Phe Asn Leu Asp Glu Gly His
 250 255 260

35 Ala Leu Arg Ile Pro Ser Gly Phe Ile Ser Tyr Ile Leu Asn Arg His
 265 270 275

Asp Asn Gln Asn Leu Arg Val Ala Lys Ile Ser Met Pro Val Asn Thr
 280 285 290

40 Pro Gly Gln Phe Glu Asp Phe Phe Pro Ala Ser Ser Arg Asp Gln Ser
 295 300 305

45 Ser Tyr Leu Gln Gly Phe Ser Arg Asn Thr Leu Glu Ala Ala Phe Asn
 310 315 320 325

Ala Glu Phe Asn Glu Ile Arg Arg Val Leu Leu Glu Glu Asn Ala Gly
 330 335 340

50 Gly Glu Gln Glu Glu Arg Gly Gln Arg Arg Ser Thr Arg Ser Ser
 345 350 355

Asp Asn Glu Gly Val Ile Val Lys Val Ser Lys Glu His Val Gln Glu
 360 365 370

55 Leu Thr Lys His Ala Lys Ser Val Ser Lys Lys Gly Ser Glu Glu Glu
 375 380 385

Asp Ile Thr Asn Pro Ile Asn Leu Arg Asp Gly Glu Pro Asp Leu Ser
390 395 400 405

5 Asn Asn Phe Gly Arg Leu Phe Glu Val Lys Pro Asp Lys Lys Asn Pro
410 415 420

Gln Leu Gln Asp Leu Asp Met Met Leu Thr Cys Val Glu Ile Lys Glu
425 430 435

10 Gly Ala Leu Met Leu Pro His Phe Asn Ser Lys Ala Met Val Ile Val
440 445 450

Val Val Asn Lys Gly Thr Gly Asn Leu Glu Leu Val Ala Val Arg Lys
15 455 460 470

Glu Gln Gln Gln Arg Gly Arg Arg Glu Gln Glu Trp Glu Glu Glu Glu
480 485 490 500

20 Glu Asp Glu Glu Glu Glu Gly Ser Asn Arg Glu Val Arg Arg Tyr Thr
505 510 515

Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met Pro Ala Ala His Pro
520 525 530

25 Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu Leu Gly Phe Gly Ile
535 540 545

Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala Gly Asp Lys Asp Asn
30 550 555 560

Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp Leu Ala Phe Pro Gly
565 570 575 580

35 Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn Gln Arg Glu Ser His
585 590 595

Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Pro Ser Ser Pro Glu Lys
40 600 605 610

Glu Asp Gln Glu Glu Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser
615 620 625

Ile Leu Lys Ala Phe Asn
45 630

(2) INFORMATION FOR SEQ ID NO: 22:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Maize
(F) TISSUE TYPE: Seeds

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Ser Ala Arg Ile Val Val Leu Leu Ala Thr Leu Leu Cys Ala
1 5 10 15

Ala Ala Ala Val Ala Ser Ser Trp Glu Asp Asp Asn His His His His
10 20 25 30

Gly Gly His Lys Ser Gly Gln Cys Val Arg Arg Cys Glu Asp Arg Pro
15 35 40 45

Trp His Gln Arg Pro Arg Cys Leu Glu Gln Cys Arg Glu Glu Glu Arg
20 50 55 60

Glu Lys Arg Gln Glu Arg Ser Arg His Glu Ala Asp Asp Arg Ser Gly
20 65 70 75 80

Glu Gly Ser Ser Glu Asp Glu Arg Glu Gln Glu Lys Glu Lys Gln Lys
25 85 90 95

Asp Arg Arg Pro Tyr Val Phe Asp Arg Arg Ser Phe Arg Arg Val Val
30 100 105 110

Arg Ser Glu Gln Gly Ser Leu Arg Val Leu Arg Pro Phe Asp Glu Val
35 115 120 125

Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Val Leu Glu
40 130 135 140

Ala Asn Pro Arg Ser Phe Val Val Pro Ser His Thr Asp Ala His Cys
45 145 150 155 160

Ile Cys Tyr Val Ala Glu Gly Glu Gly Val Val Thr Thr Ile Glu Asn
40 165 170 175 180

Gly Glu Arg Arg Ser Tyr Thr Ile Lys Gln Gly His Val Phe Val Ala
45 185 190 195

Pro Ala Gly Ala Val Thr Tyr Leu Ala Asn Thr Asp Gly Arg Lys Lys
50 200 205 210

Leu Val Ile Thr Lys Ile Leu His Thr Ile Ser Val Pro Gly Glu Phe
55 215 220 225

Gln Phe Phe Phe Gly Pro Gly Gly Arg Asn Pro Glu Ser Phe Leu Ser
50 230 235 240 245

Ser Phe Ser Lys Ser Ile Gln Arg Ala Ala Tyr Lys Thr Ser Ser Asp
55 250 255 260

Arg Leu Glu Arg Leu Phe Gly Arg His Gly Gln Asp Lys Gly Ile Ile

265

270

275

Val Arg Ala Thr Glu Glu Gln Thr Arg Glu Leu Arg Arg His Ala Ser
 280 285 290

5

Glu Gly Gly His Gly Pro His Trp Pro Leu Pro Pro Phe Gly Glu Ser
 295 300 305

Arg Gly Pro Tyr Ser Leu Leu Asp Gln Arg Pro Ser Ile Ala Asn Gln
 10 310 315 320 325

His Gly Gln Leu Tyr Glu Ala Asp Ala Arg Ser Phe His Asp Leu Ala
 330 335 340

15 Glu His Asp Val Ser Val Ser Phe Ala Asn Ile Thr Ala Gly Ser Met
 345 350 355

Ser Ala Pro Leu Phe Asn Thr Arg Ser Phe Lys Ile Ala Tyr Val Pro
 20 360 365 370

Asn Gly Lys Gly Tyr Ala Glu Ile Val Cys Pro His Arg Gln Ser Gln
 375 380 385

25 Gly Gly Glu Ser Glu Arg Glu Arg Asp Lys Gly Arg Arg Ser Glu Glu
 390 395 400 405

Glu Glu Glu Glu Ser Ser Glu Glu Gln Glu Glu Ala Gly Gln Gly Tyr
 410 415 420

30 His Thr Ile Arg Ala Arg Leu Ser Pro Gly Thr Ala Phe Val Val Pro
 425 430 435

Ala Gly His Pro Phe Val Ala Val Ala Ser Arg Asp Ser Asn Leu Gln
 35 440 445 450

Ile Val Cys Phe Glu Val His Ala Asp Arg Asn Glu Lys Val Phe Leu
 455 460 470

40 Ala Gly Ala Asp Asn Val Leu Gln Lys Leu Asp Arg Val Ala Lys Ala
 480 485 490 500

Leu Ser Phe Ala Ser Lys Ala Glu Glu Val Asp Glu Val Leu Gly Ser
 505 510 515

45 Arg Arg Glu Lys Gly Phe Leu Pro Gly Pro Glu Glu Ser Gly Gly His
 520 525 530

Glu Glu Arg Glu Gln Glu Glu Glu Arg Glu Glu Arg His Gly Gly
 535 540 545

50 Arg Gly Glu Arg Glu Arg His Gly Arg Glu Glu Arg Glu Lys Glu Glu
 550 555 560

55 Glu Arg Glu Gly Arg His Gly Gly Arg Glu Glu Arg Glu Glu Glu Glu
 565 570 575 580

60

Arg His Gly Arg Gly Arg Arg Glu Glu Val Ala Glu Thr Leu Met Arg
585 590 595

Met Val Thr Ala Arg Met
5 600

(2) INFORMATION FOR SEQ ID NO: 23:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: Maize
(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

25 Arg Ser Gly Arg Gly Glu Cys Arg Arg Gln Cys Leu Arg Arg His Glu
1 5 10 15

Gly Gln Pro Trp Glu Thr Gln Glu Cys Met Arg Arg Cys Arg Arg Arg
20 25 30

30 Gly

(2) INFORMATION FOR SEQ ID NO: 24:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: Barley
(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

50 Met Ala Thr Arg Ala Lys Ala Thr Ile Pro Leu Leu Phe Leu Leu Gly
1 5 10 15

Thr Ser Leu Leu Phe Ala Ala Ala Val Ser Ala Ser His Asp Asp Glu
20 25 30

55 Asp Asp Arg Arg Gly Gly His Ser Leu Gln Gln Cys Val Gln Arg Cys
35 40 45

Arg Gln Glu Arg Pro Arg Tyr Ser His Ala Arg Cys Val Gln Glu Cys
50 55 60

5 Arg Asp Asp Gln Gln Gln His Gly Arg His Glu Gln Glu Glu Glu Gln
65 70 75 80

Gly Arg Gly Arg Gly Trp His Gly Glu Gly Glu Arg Glu Glu Glu His
10 85 90 95

Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu His
100 105 110

15 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
115 120 125

Gly Arg Gly His Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
130 135 140

20 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Glu
145 150 155 160

Gly Arg Gly Arg Gly Arg Arg Gly Glu Gly Glu Arg Asp Glu Glu Gln
25 165 170 175 180

Gly Asp Ser Arg Arg Pro Tyr Val Phe Gly Pro Arg Ser Phe Arg Arg
185 190 195

30 Ile Ile Gln Ser Asp His Gly Phe Val Arg Ala Leu Arg Pro Phe Asp
200 205 210

Gln Val Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Ile
215 220 225

35 Met Glu Val Asn Pro Arg Ala Phe Val Val Pro Gly Phe Thr Asp Ala
230 235 240 245

Asp Gly Val Gly Tyr Val Ala Gln Gly Glu Gly Val Leu Thr Val Ile
40 250 255 260

Glu Asn Gly Glu Lys Arg Ser Tyr Thr Val Lys Glu Gly Asp Val Ile
265 270 275

45 Val Ala Pro Ala Gly Ser Ile Met His Leu Ala Asn Thr Asp Gly Arg
280 285 290

Arg Lys Leu Val Ile Ala Lys Ile Leu His Thr Ile Ser Val Pro Gly
295 300 305

50 Lys Phe Gln Phe Leu Ser Val Lys Pro Leu Leu Ala Ser Leu Ser Lys
310 315 320 325

Arg Val Leu Arg Ala Ala Phe Lys Thr Ser Asp Glu Arg Leu Glu Arg
55 330 335 340

Leu Phe Asn Gln Arg Gln Gly Gln Glu Lys Thr Arg Ser Val Ser Ile

345

350

355

Val Arg Ala Ser Glu Glu Gln Leu Arg Glu Leu Arg Arg Glu Ala Ala
360 365 370

5 Glu Gly Gly Gln Gly His Arg Trp Pro Leu Pro Pro Phe Arg Gly Asp
375 380 385

10 Ser Arg Asp Thr Phe Asn Leu Leu Glu Gln Arg Pro Lys Ile Ala Asn
390 395 400 405

Arg His Gly Arg Leu Tyr Glu Ala Asp Ala Arg Ser Phe His Ala Leu
410 415 420

15 Ala Asn Gln Asp Val Arg Val Ala Val Ala Asn Ile Thr Pro Gly Ser
425 430 435

Met Thr Ala Pro Tyr Leu Asn Thr Gln Ser Phe Lys Leu Ala Val Val
440 445 450

20 Leu Glu Gly Glu Gly Glu Val Gln Ile Val Cys Pro His Leu Gly Arg
455 460 470

25 Glu Ser Glu Ser Glu Arg Glu His Gly Lys Gly Arg Arg Arg Glu Glu
480 485 490 500

Glu Glu Asp Asp Gln Arg Gln Gln Arg Arg Arg Gly Ser Glu Ser Glu
505 510 515

30 Ser Glu Glu Glu Glu Gln Gln Arg Tyr Glu Thr Val Arg Ala Arg
520 525 530

Val Ser Arg Gly Ser Ala Phe Val Val Pro Pro Gly His Pro Val Val
535 540 545

35 Glu Ile Ser Ser Ser Gln Gly Ser Ser Asn Leu Gln Val Val Cys Phe
550 555 560

40 Glu Ile Asn Ala Glu Arg Asn Glu Arg Val Trp Leu Ala Gly Arg Asn
565 570 575 580

Asn Val Ile Gly Lys Leu Gly Ser Pro Ala Gln Glu Leu Thr Phe Gly
585 590 595

45 Arg Pro Ala Arg Glu Val Gln Glu Val Phe Arg Ala Gln Asp Gln Asp
600 605 610

Glu Gly Phe Val Ala Gly Pro Glu Gln Gln Ser Arg Glu Gln Glu Gln
615 620 625

50 Glu Gln Glu Arg His Arg Arg Gly Asp Arg Gly Arg Gly Asp Glu
630 635 640

55 Ala Val Glu Thr Phe Leu Arg Met Ala Thr Gly Ala Ile
645 650 655

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: Soybean (*Glycine max*)
 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Met Arg Ala Arg Phe Pro Leu Leu Leu Leu Gly Leu Val Phe Leu
1 5 10 15

Ala Ser Val Ser Val Ser Phe Gly Ile Ala Tyr Trp Glu Lys Glu Asn
20 25 30

Pro Lys His Asn Lys Cys Leu Gln Ser Cys Asn Ser Glu Arg Asp Ser
25 35 40 45

Tyr Arg Asn Gln Ala Cys His Ala Arg Cys Asn Leu Leu Lys Val Glu
50 55 60

Lys Glu Glu Cys Glu Glu Gly Glu Ile Pro Arg Pro Arg Pro Arg Pro
30 65 70 75 80

Gln His Pro Glu Arg Glu Pro Gln Gln Pro Gly Glu Lys Glu Glu Asp
35 85 90 95

Glu Asp Glu Gln Pro Arg Pro Ile Pro Phe Pro Arg Pro Gln Pro Arg
40 100 105 110

Gln Glu Glu Glu His Glu Gln Arg Glu Glu Gln Glu Trp Pro Arg Lys
45 115 120 125

Glu Glu Lys Arg Gly Glu Lys Gly Ser Glu Glu Asp Glu Asp Glu
50 130 135 140

Asp Glu Glu Gln Asp Glu Arg Gln Phe Pro Phe Pro Arg Pro Pro His
55 145 150 155 160

Gln Lys Glu Glu Arg Asn Glu Glu Glu Asp Glu Asp Glu Glu Gln Gln
60 165 170 175 180

Arg Glu Ser Glu Glu Ser Glu Asp Ser Glu Leu Arg Arg His Lys Asn
65 185 190 195

Lys Asn Pro Phe Leu Phe Gly Ser Asn Arg Phe Glu Thr Leu Phe Lys
70 200 205 210

| | | | | |
|----|---|-----|-----|-----|
| | Asn Gln Tyr Gly Arg Ile Arg Val Leu Gln Arg Phe Asn Gln Arg Ser | | | |
| | 215 | 220 | 225 | |
| 5 | Pro Gln Leu Gln Asn Leu Arg Asp Tyr Arg Ile Leu Glu Phe Asn Ser | | | |
| | 230 | 235 | 240 | 245 |
| | Lys Pro Asn Thr Leu Leu Leu Pro Asn His Ala Asp Ala Asp Tyr Leu | | | |
| | 250 | 255 | 260 | |
| 10 | Ile Val Ile Leu Asn Gly Thr Ala Ile Leu Ser Leu Val Asn Asn Asp | | | |
| | 265 | 270 | 275 | |
| | Asp Arg Asp Ser Tyr Arg Leu Gln Ser Gly Asp Ala Leu Arg Val Pro | | | |
| | 280 | 285 | 290 | |
| 15 | Ser Gly Thr Thr Tyr Tyr Val Val Asn Pro Asp Asn Asn Glu Asn Leu | | | |
| | 295 | 300 | 305 | |
| 20 | Arg Leu Ile Thr Leu Ala Ile Pro Val Asn Lys Pro Gly Arg Phe Glu | | | |
| | 310 | 315 | 320 | 325 |
| | Ser Phe Phe Leu Ser Ser Thr Glu Ala Gln Gln Ser Tyr Leu Gln Gly | | | |
| | 330 | 335 | 340 | |
| 25 | Phe Ser Arg Asn Ile Leu Glu Ala Ser Tyr Asp Thr Lys Phe Glu Glu | | | |
| | 345 | 350 | 355 | |
| | Ile Asn Lys Val Leu Phe Ser Arg Glu Glu Gly Gln Gln Gly Glu | | | |
| | 360 | 365 | 370 | |
| 30 | Gln Arg Leu Gln Glu Ser Val Ile Val Glu Ile Ser Lys Glu Gln Ile | | | |
| | 375 | 380 | 385 | |
| 35 | Arg Ala Leu Ser Lys Arg Ala Lys Ser Ser Arg Lys Thr Ile Ser | | | |
| | 390 | 395 | 400 | 405 |
| | Ser Glu Asp Lys Pro Phe Asn Leu Arg Ser Arg Asp Pro Ile Tyr Ser | | | |
| | 410 | 415 | 420 | |
| 40 | Asn Lys Leu Gly Lys Phe Phe Glu Ile Thr Pro Glu Lys Asn Pro Gln | | | |
| | 425 | 430 | 435 | |
| | Leu Arg Asp Leu Asp Ile Phe Leu Ser Ile Val Asp Met Asn Glu Gly | | | |
| | 440 | 445 | 450 | |
| 45 | Ala Leu Leu Leu Pro His Phe Asn Ser Lys Ala Ile Val Ile Leu Val | | | |
| | 455 | 460 | 470 | |
| 50 | Ile Asn Glu Gly Asp Ala Asn Ile Glu Leu Val Gly Leu Lys Glu Gln | | | |
| | 480 | 485 | 490 | 500 |
| | Gln Gln Glu Gln Gln Glu Glu Gln Pro Leu Glu Val Arg Lys Tyr | | | |
| | 505 | 510 | 515 | |
| 55 | Arg Ala Glu Leu Ser Glu Gln Asp Ile Phe Val Ile Pro Ala Gly Tyr | | | |
| | 520 | 525 | 530 | |

Pro Val Val Val Asn Ala Thr Ser Asn Leu Asn Phe Phe Ala Ile Gly
535 540 545

5 Ile Asn Ala Glu Asn Asn Gln Arg Asn Phe Leu Ala Gly Ser Gln Asp
550 555 560

Asn Val Ile Ser Gln Ile Pro Ser Gln Val Gln Glu Leu Ala Phe Pro
565 570 575 580
10 Gly Ser Ala Gln Ala Val Glu Lys Leu Leu Lys Asn Gln Arg Glu Ser
585 590 595

Tyr Phe Val Asp Ala Gln Pro Lys Lys Lys Glu Glu Gly Asn Lys Gly
15 600 605 610

Arg Lys Gly Pro Leu Ser Ser Ile Leu Arg Ala Phe Tyr
615 620 625

20 (2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Stenocarpus sinuatus
- (F) TISSUE TYPE: Seeds

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Lys Glu Asp His Gln Phe Glu Thr Arg Gly Glu Ile Leu Glu Cys
1 5 10 15

40 Tyr Arg Leu Cys Gln Gln Gln
20

45 (28) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Stenocarpus sinuatus
- (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

5 Gln Lys His Arg Ser Gln Ile Leu Gly Cys Tyr Leu Xxx cys Gln Gln
1 5 10 15

Leu

10 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Stenocarpus sinuatus
- (F) TISSUE TYPE: Seeds

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

20 Leu Asp Pro Ile Arg Gln Gln Leu Cys Gln Met Arg Cys Gln Gln
1 5 10 15

30 Gln Glu Lys Asp Pro Arg Gln Gln Gln Cys Lys
20 25